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Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: Connective Tissue Growth Factor - 2

Inventors (please provide full names): Li et al Point of Contact: Mona Smith

Earliest Priority Filing Date: 7/8/99 Technical Info. Specialist
CM1 12C14 Tel: 308-3278

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

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(2)

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M

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part 2

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Type of Search

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Search History**Today's Date: 1/8/2001**

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USPT,JPAB,EPAB,DWPI,TDBD	(li-haodong.in. or li-h\$.in.) and ctgf	5	<u>L5</u>
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USPT,JPAB,EPAB,DWPI,TDBD	connective adj tissue adj growth adj factor\$	66	<u>L1</u>

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S2	1209	CONNECTIVE(W) TISSUE(W) GROWTH(W) FACTOR?
S3	25	S2(S)ISOFORM?
S4	7	RD (unique items)
S5	2	AU=(ADAMS MARK OR ADAMS,M? OR ADAMS M? OR ADAMS, MARK) AND CTGF?
S6	2	RD (unique items)
S7	3	AU=(LI HAODONG OR LI, HAODONG OR LI H? OR LI, H?) AND CTGF
S8	3	RD (unique items)

Tue Jan 9 11:37:33 2001

us-09-348-815-2.rpr

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OM protein - protein search, using sw model

Run on: January 8, 2001, 10:36:00 ; Search time 17.32 Seconds
(without alignments)
1493.658 Million cell updates/sec

Title: US-09-348-815-2
Perfect score: 2115
Sequence: 1 MSSRIARALALVTLHLTR.....ANEAFFYFLNDIHKFRD 381

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues
Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_66: *
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2: PIR2: *
3: PIR3: *
4: PIR4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1938	91.6	379	2 A35669	gene CYR61 protein
2	1699	80.3	375	2 A41428	CEF-10 protein pre
3	956.5	45.2	348	2 A40578	beta IG-M2 protein
4	952.5	45.0	348	2 A53228	flisp-12 protein pr
5	951	45.0	349	2 A40551	connective tissue
6	855.5	40.4	351	2 S20078	NOV protein - chic
7	834.5	39.5	357	2 I38069	gene novh protein
8	175.5	8.3	1620	2 T27283	hypothetical prote
9	174	8.2	1111	2 T26972	hypothetical prote
10	159	7.5	1700	2 S08167	Balbani ring 3 pr
11	156	7.4	1574	2 T13954	MEGF6 protein - ra
12	153	7.2	837	2 A42112	muslin-like peptide
13	152.5	7.2	1178	1 A39804	thrombospondin pre
14	152	7.2	5376	2 T42215	zonadhesin - mouse
15	147.5	7.0	1170	2 A53612	laminin Blk chain
16	145	6.9	601	2 T22025	hypothetical prote
17	144	6.8	1984	2 T09059	notch4 - mouse
18	142	6.7	1025	2 T42626	secreted leucine-r
19	141.5	6.7	1034	2 JC5598	muslin - rat
20	141.5	6.7	1101	2 T16840	hypothetical prote
21	141.5	6.7	13288	2 T03099	muslin, submaxillar
22	141	6.7	3020	2 A43932	muslin 2 precursor,
23	140.5	6.6	2703	1 A24420	notch protein - fr
24	139	6.6	1042	2 A57534	muslin 5AC (clone L
25	138	6.5	251	2 A55035	cysteine-rich prot
26	138	6.5	2437	2 S18488	transmembrane prot
27	136	6.4	2531	2 T42629	notch protein homo
28	136	6.4	4135	2 T42629	tenascin-X - bovin
29	135	6.4	473	2 A56175	adhesive plaque pr

30 135 6.4 1168 2 I56985 kalinin Bl - mou
31 134 6.3 1056 2 A53767 mucin MUC5B, tral
32 134 6.3 3002 2 A47221 fibrillin 1 precur
33 133.5 6.3 1106 2 T13938 gene shuttle craft
34 133.5 6.3 1480 2 A36665 slit protein 1 pre
35 133.5 6.3 1955 1 AGCH aglin precursor -
36 133 6.3 1170 2 A40558 thrombospondin 1 p
37 133 6.3 1296 2 T16859 hypothethical prote
38 133 6.3 2813 1 VNHU von Willebrand fac
39 133 6.3 3106 1 S53868 laminin alpha-2 ch
40 133 6.3 3672 2 T23433 hypothethical prote
41 132.5 6.3 3704 2 T37316 probabable laminin a
42 132.5 6.3 1106 2 T44598 hypothethical prote
43 132.5 6.3 1847 2 T18308 probabable vitelloge
44 132.5 6.3 2555 2 A40043 notch protein homo
45 132 6.2 2823 2 T23064 hypothethical prote

ALIGNMENTS

RESULT 1
A35669
gene CYR61 protein precursor - mouse
C:Species: Mus musculus (house mouse)
C>Date: 28-Sep-1990 #sequence_revision 18-Nov-1992 #text_change 05-Nov-1999
C:Accession: A35669; I48319; S16446
R:O'Brien, T.P.; Yang, G.P.; Sanders, L.; Lau, L.F.
Mol. Cell. Biol. 10, 3569-3577, 1990
A:Title: Expression of cyr61, a growth factor-inducible immediate-early gene.
A:Reference number: A35669; MUID:90287146
A:Accession: A35669
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-379 <ORF>
A:Cross-references: GB:M32490; NID:gl92909; PIDN:AAA37512.1; PID:g309206
A:Note: the authors translated the codon GAT for residue 337 as Gln
R:Latickic, B.V.; O'Brien, T.P.; Lau, L.F.
Nucleic Acids Res. 19, 3261-3267, 1991
A:Title: Promoter function and structure of the growth factor-inducible immediate ear
A:Reference number: I48319; MUID:91288203
A:Accession: I48319
A:Status: translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-379 <RES>
A:Cross-references: EMBL:X56790; NID:g50632; PIDN:CAA40109.1; PID:g50633
A:Note: the authors did not translate the codon for residue 108
A:Note: the authors translated the codon GAT for residue 337 as Gln
C:Genetics:
A:Gene: CYR61
A:Introns: 21/3; 93/1; 208/1; 279/3
A:Superfamily: von Willebrand factor type C repeat homology
F:99-166/Domain: von Willebrand factor type C repeat homology <YWC>

Query Match 91.6% Score 1938; DB 2; Length 379;
Best Local Similarity 91.4%; Pred. No. 1.2e-135;
Matches 350; Conservative 9; Mismatches 18; Indels 6; Gaps 2;

Qy 1 MSSRIARALALVTLHLTRALSTCPAACHCPLAEPKAPGVGLVRDGGCCCKVCAKQL 60
Db 1 MSSFTFRTLAVAVTLLHLTRALSTCPAACHCPLAEPKAPGVGLVRDGGCCCKVCAKQL 60
Qy 61 NEDCSKTPCDHTKGLCNFGASSTALKGICRAOSEGRPCPEYNSRIYONGESFPNCKHQ 120
Db 61 NEDCSKTPCDHTKGLCNFGASSTALKGICRAOSEGRPCPEYNSRIYONGESFPNCKHQ 120
Qy 121 CTCIDGAVGCGIPLCPQELSLNLGCPNRLVKYVTCGCEEWVCDSDSIKDDDDDL-- 178
Db 121 CTCIDGAVGCGIPLCPQELSLNLGCPNRLVKYVTCGCEEWVCDSDSIKDDDDDL-- 178
Qy 181 KELGFDASEVELTRNNELIAGKSSLRPLVFGMEPRILYNPL--OGQKCIIVOTTWSQ 238
Db 181 KELGFDASEVELTRNNELIAGKSSLRPLVFGMEPRILYNPL--OGQKCIIVOTTWSQ 238

Db 179 --LGLDASEVELTRNNELIAGKSSLKRLPVFGTEPRVLFNPLHAQCKQKIVQTTWSQ 236
 QY 239 CSKTCGGTISTRTVNDNPECLVETRICVPCGPQVYSSLLKGGKCKSKTKKSPVPVF 298
 Db 237 CSKSCGGTISTRTVNDNPECLVETRICVPCGPQVYSSLLKGGKCKSKTKKSPVPVF 296
 QY 299 TYAGCLSVKKYRKYPCGSCVDGRCTPQTRTVKMRFCEDGETFSKNVMIQSCCKNYN 358
 Db 297 TYAGSSVKKYRKYPCGSCVDGRCTPQTRTVKMRFCEDGETFSKNVMIQSCCKNYN 356
 QY 359 CPHANEAAFPFYRLFNDFHFRD 381
 Db 357 CPHNEASFRLYSLFNDFHFRD 379

RESULT 2
 A41428
 CEF-10 protein precursor - chicken
 C:Species: Gallus gallus (chicken)
 C:Date: 03-Apr-1992 #sequence_revision 03-Apr-1992 #text_change 21-Jul-2000
 R:Accession: A41428
 R:Simmons, D.L.; Levy, D.B.; Yannoni, Y.; Erikson, R.L.
 Proc. Natl. Acad. Sci. U.S.A. 86, 1178-1182, 1989
 A:Title: Identification of a phorbol ester-repressible v-src-inducible gene.
 A:Reference number: A41428; MUID:89145206
 A:Accession: A41428
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-375 <Sim>
 A:Cross-references: GB:J04496; NID:g211435; PIDN:AAA48661.1; PID:g211436

Query Match 80.3%; Score 1699; DB 2; Length 375;
 Best Local Similarity 81.2%; Pred. No. 4.8e-118;
 Matches 312; Conservative 19; Mismatches 41; Indels 12; Gaps 7;

QY 1 MSSRIARALALVTVLLHL-TRIAL-STCPAACHCPL-APKCAPGVGLVDRDGGCCCKVCA 59
 Db 1 MGSAGARP-ALAAALLCLARLALGSPCAVQCPCPAAPOCAPGVGLVDRDGGCCCKVCA 59
 QY 60 LNECDSTQPCDHTKGLGECNFGASSTALKICRAQSEGRPCPEYNSRIYONGESFQPNCKH 119
 Db 60 LNECDSTQPCDHTKGLGECNFGASSTALKICRAQSEGRPCPEYNSRIYONGESFQPNCKH 119
 QY 120 QCTCIDGAVGCIPLCPOELSLPNLGCPNPLVYKVTGOCCEWVCDSDIKDPMEDQGLL 179
 Db 120 QCTCIDGAVGCIPLCPOELSLPNLGCPNPLVYKVTGOCCEWVCDSDIKDPMEDQGLL 179
 QY 180 GKEIGFDASEVELTRNNELIAGKSSLKRLPVFGMEP--RILYNPLOGQKCIQVQTTWS 237
 Db 178 SKEFGLDASGELTRNNELIAGKSSLKRLPVFGMEP--RILYNPLOGQKCIQVQTTWS 232
 QY 238 QCSKTCTGISTRTVNDNPECLVETRICVPCGPQVYSSLLKGGKCKSKTKKSPVPVF 297
 Db 233 QCSKTCTGISTRTVNDNPECLVETRICVPCGPQVYSSLLKGGKCKSKTKKSPVPVF 292
 QY 298 FYAGCLSVKKYRKYPCGSCVDGRCTPQTRTVKMRFCEDGETFSKNVMIQSCCKNY 357
 Db 293 FYAGSSVKKYRKYPCGSCVDGRCTPQTRTVKMRFCEDGETFSKNVMIQSCCKNY 352
 QY 358 NCPHANEAAFPFYRLFNDFHFRD 381
 Db 353 NCPHANEAAFPFYRLFNDFHFRD 375

RESULT 3
 A40578
 beta IG-M2 protein precursor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 06-Mar-1992 #sequence_revision 06-Mar-1992 #text_change 05-Nov-1999
 R:Accession: A40578
 R:Chinn, A.; Chinn, J.; Neubauer, M.; Purchio, A.F.
 Mol. Biol. Cell. 10, 293-300, 1991

A:Title: Identification of a gene family regulated by transforming growth factor-beta
 A:Reference number: A40578; MUID:91229699
 A:Accession: A40578
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-348 <BRU>
 A:Cross-references: GB:M80263; NID:g201945; PIDN:AAA73135.1; PID:g201946

Query Match 45.2%; Score 956.5; DB 2; Length 348;
 Best Local Similarity 46.9%; Pred. No. 2.2e-63;
 Matches 179; Conservative 56; Mismatches 106; Indels 41; Gaps 8;

QY 1 MSSRIARALALVTVLLHL-TRIAL-STCPAACHCPL-APKCAPGVGLVDRDGGCCCKVCA 57
 Db 1 MLASVAGPISLALVLLALCTRPATGQCSAQCOCACAAEAPHCAPAGVSLVLDGGCCCRVCA 60
 QY 58 KOLNEDCSKTQPCDHTKGLGECNFGASSTALKICRAQSEGRPCPEYNSRIYONGESFQPNCK 117
 Db 61 KOLGELCTERDPCDHTKGLGECNFGASSTALKICRAQSEGRPCPEYNSRIYONGESFQPNCK 119
 QY 118 KQCTCIDGAVGCIPLCPOELSLPNLGCPNPLVYKVTGOCCEWVCDSDIKDPMEDQGL 177
 Db 120 KQCTCIDGAVGCIPLCPOELSLPNLGCPNPLVYKVTGOCCEWVCDSDIKDPMEDQGL 177
 QY 178 LIGKELGFDASEVELTRNNELIAGKSSLKRL-PVFGMEPRILYNPLOGQKCIQVQTTWS 236
 Db 169 -----KDRTAGVPALAAAYRLEDTFGDPTMM-----RANCLVQTTWS 205
 QY 237 SOCSKTCTGISTRTVNDNPECLVETRICVPCGPQVYSSLLKGGKCKSKTKKSPVPVF 296
 Db 206 SACSXTCTGISTRTVNDNPECLVETRICVPCGPQVYSSLLKGGKCKSKTKKSPVPVF 265
 QY 297 RFTYAGCLSVKKYRKYPCGSCVDGRCTPQTRTVKMRFCEDGETFSKNVMIQSCCKNY 356
 Db 266 KFELSGCTSVTYRAKFGVCTDGRCCPHRTTLLPVFECGPDGEIMKKMMFIKTCACH 325
 QY 357 YNCPHANEAAFPFY--RLFNDF 376
 Db 326 YNCPGDNDIFESLYRKYMGDM 347

RESULT 4
 A53228
 fisp-12 protein precursor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 05-Nov-1999
 R:Accession: A53228
 R:Rybeck, R.P.; Macdonald-Bravo, H.; Mattei, M.G.; Bravo, R.
 Cell Growth Differ. 2, 225-233, 1991
 A:Title: Structure, mapping, and expression of fisp-12, a growth factor-inducible gene
 A:Reference number: A53228
 A:Accession: A53228
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-348 <RYS>
 A:Cross-references: GB:M70641; NID:g193313; PIDN:AAA37627.1; PID:g193314
 C:Genetics:
 A:Gene: fisp-12

Query Match 45.0%; Score 952.5; DB 2; Length 348;
 Best Local Similarity 46.6%; Pred. No. 4.4e-63;
 Matches 178; Conservative 57; Mismatches 106; Indels 41; Gaps 8;

QY 1 MSSRIARALALVTVLLHL-TRIAL-STCPAACHCPL-APKCAPGVGLVDRDGGCCCKVCA 57
 Db 1 MLASVAGPISLALVLLALCTRPATGQCSAQCOCACAAEAPHCAPAGVSLVLDGGCCCRVCA 60
 QY 58 KOLNEDCSKTQPCDHTKGLGECNFGASSTALKICRAQSEGRPCPEYNSRIYONGESFQPNCK 117
 Db 61 KOLGELCTERDPCDHTKGLGECNFGASSTALKICRAQSEGRPCPEYNSRIYONGESFQPNCK 119

INTERPRO: IPR000867; -
DR INTERPRO: IPR000884; -
DR INTERPRO: IPR001007; -
DR PFAM: PF00007; Cys_knot; 1.
DR PFAM: PF00219; IGFBP; 1.
DR PFAM: PF00090; tsp_1; 1.
DR PFAM: PF00093; vwc; 1.
DR PROSITE: PS00222; IGF_BINDING; 1.
DR PROSITE: PS01185; CTCK_1; 1.
DR PROSITE: PS01225; CTCK_2; 1.
DR PROSITE: PS01208; WMFC; 1.
KW Growth factor binding; Signal.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 381 CYR61 PROTEIN.
FT DOMAIN 98 164 WMFC.
FT DISULFID 286 360 CTCK.
FT DISULFID 286 323 BY SIMILARITY.
FT DISULFID 303 337 BY SIMILARITY.
FT DISULFID 314 353 BY SIMILARITY.
FT DISULFID 317 355 BY SIMILARITY.
FT DISULFID 322 359 BY SIMILARITY.
FT CONFLICT 210 210 L -> I (IN REF. 4).
FT CONFLICT 220 220 L -> R (IN REF. 4).
SQ SEQUENCE 381 AA; 42026 MW; FC0BD39C078CA0B1 CRC64;

Query Match 100.0%; Score 2115; DB 1; Length 381;
Best Local Similarity 100.0%; Pred. No. 3.9e-154;
Matches 381; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSSRIARALVLTLLHLTRALSTCPAACHCPLKAPKAPGVGLVDRGCGCKVCAKQL 60
DB 1 MSSRIARALVLTLLHLTRALSTCPAACHCPLKAPKAPGVGLVDRGCGCKVCAKQL 60
QY 61 NEDCSKTOPCDHTKGLNCFNFGASTALGICRAQSGRCPCEYNSRIYQNGESFQPNCKHQ 120
DB 61 NEDCSKTOPCDHTKGLNCFNFGASTALGICRAQSGRCPCEYNSRIYQNGESFQPNCKHQ 120
QY 121 CTCIDGAVGICPLCPQELSLPGLNCGPNRLVKTGCCSEWVCEWDESDIKDPMEDQDGLLG 180
DB 121 CTCIDGAVGICPLCPQELSLPGLNCGPNRLVKTGCCSEWVCEWDESDIKDPMEDQDGLLG 180
QY 181 KELGFDASEVELTRNELLAVKGSLLKPLVFGMEPRILYNPLOGKCIQVOTTSWQCS 240
DB 181 KELGFDASEVELTRNELLAVKGSLLKPLVFGMEPRILYNPLOGKCIQVOTTSWQCS 240
QY 241 KTCGTGISTRTVNDNPECLVETRICVRCPCQPVYSSLLKKGKCKSKTKKSPVVRFTY 300
DB 241 KTCGTGISTRTVNDNPECLVETRICVRCPCQPVYSSLLKKGKCKSKTKKSPVVRFTY 300
QY 301 AGCLSVKRYKPKYKCGVDRGCTPQLTRTVKMRFCEDGETFSKNVMQSKCNYNCP 360
DB 301 AGCLSVKRYKPKYKCGVDRGCTPQLTRTVKMRFCEDGETFSKNVMQSKCNYNCP 360
QY 361 HANEAAFPYRLFNDIHKFRD 381
DB 361 HANEAAFPYRLFNDIHKFRD 381

RESULT 2
CYR6_MOUSE
ID CYR6_MOUSE STANDARD; PRT; 379 AA.
AC P18406;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE CYR61 PROTEIN PRECURSOR (3CH61).
GN CYR61 OR IGFBP10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN-BALB/C; TISSUE=FIBROBLAST;
RX MEDLINE=90287146; PubMed=2355916;
RA O'Brien T.P., Yang G.P., Sanders L., Lau L.F.;
RT "Expression of cyr61, a growth factor-inducible immediate-early
gene.";
RL Mol. Cell. Biol. 10:3569-3577(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-AJ; TISSUE=EMBRYONIC FIBROBLAST;
RX MEDLINE=91288203; PubMed=2062642;
RA Latinkic B.V., O'Brien T.P., Lau L.F.;
RT "Promoter function and structure of the growth factor-inducible
nucleic acids early gene cyr61.";
RL Nucleic Acids Res. 19:3261-3267(1991).
CC -1- FUNCTION: MAY ACT AS ONE OF THE MANY GROWTH FACTOR-BINDING
PROTEINS; PROMOTES PROLIFERATION, MIGRATION AND ADHESION.
CC -1- TISSUE SPECIFICITY: LOW IN KIDNEY, ADRENAL GLAND, TESTES, BRAIN,
AND OVARY, MODERATE IN HEART, UTERUS, AND SKELETAL MUSCLE, HIGHEST
IN LUNG.
CC -1- DEVELOPMENTAL STAGE: EXPRESSED FROM G(0)/G(1) THROUGH MID-G(1) IN
NORMAL CELLS, AND AT A CONSTANT LEVEL IN RAPIDLY GROWING CELLS.
CC -1- INDUCTION: BY GROWTH FACTORS.
CC -1- SIMILARITY: BELONGS TO THE INSULIN-LIKE GROWTH FACTOR BINDING
PROTEIN FAMILY. CEF-10/CYR61/CFEG/FISP-12/NOV PROTEIN SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 1 WMFC DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 C-TERMINAL CYSTEINE KNOT-LIKE DOMAIN (CTCK).
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CC -----
DR EMBL: M32490; AAA37512.1; -
DR EMBL: X56790; CAA40109.1; -
DR PIR: A35669; A35669.
DR MGD: MGI:88613; CYR61.
DR INTERPRO: IPR000359; -
DR INTERPRO: IPR000867; -
DR INTERPRO: IPR000884; -
DR PFAM: PF00007; Cys_knot; 1.
DR PFAM: PF00219; IGFBP; 1.
DR PFAM: PF00090; tsp_1; 1.
DR PFAM: PF00093; vwc; 1.
DR PROSITE: PS00222; IGF_BINDING; 1.
DR PROSITE: PS01185; CTCK_1; 1.
DR PROSITE: PS01225; CTCK_2; 1.
DR PROSITE: PS01208; WMFC; 1.
KW Growth factor binding; Signal.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 379 CYR61 PROTEIN.
FT DOMAIN 98 164 WMFC.
FT DOMAIN 284 358 CTCK.
FT DISULFID 284 321 BY SIMILARITY.
FT DISULFID 301 335 BY SIMILARITY.
FT DISULFID 312 351 BY SIMILARITY.
FT DISULFID 315 353 BY SIMILARITY.
FT DISULFID 320 357 BY SIMILARITY.
SQ SEQUENCE 379 AA; 41709 MW; FA6B5014B56A8EE9 CRC64;

Query Match 91.6%; Score 1938; DB 1; Length 379;
Best Local Similarity 91.4%; Pred. No. 1.1e-140;
Matches 350; Conservative 9; Mismatches 18; Indels 6; Gaps 2;

QY 1 MSSRIARALVLTLLHLTRALSTCPAACHCPLKAPKAPGVGLVDRGCGCKVCAKQL 60
DB 1 MSSRIARALVLTLLHLTRALSTCPAACHCPLKAPKAPGVGLVDRGCGCKVCAKQL 60
QY 61 NEDCSKTOPCDHTKGLNCFNFGASTALGICRAQSGRCPCEYNSRIYQNGESFQPNCKHQ 120

Db 61 NEDCSKTQPCDHTKGLGECNFGASSTALGICRAQSEGRPCPEYNSRIYQNGESFPNCKHQ 120
 QY 121 CTCIDGAVGCIPLCPQELSLPGLGCPNPLVKTGQCCCEWVCDSDSIKDPMEDQDGLLG 180
 Db 121 CTCIDGAVGCIPLCPQELSLPGLGCPNPLVKTGQCCCEWVCDSDSIKDSLDDQDDL-- 178
 QY 181 KELGFDASEVELTRNNELIAGVKGSSLKRLPVFGMEPRILYNPL--QGKCIQVQTTWSQ 238
 Db 179 --LGLDASEVELTRNNELIAGVKGSSLKRLPVFGTEPRVLFNPLHAGQKCIQVQTTWSQ 236
 QY 239 CSKTCGTGISTRTVNDNPECLRVKTRICEVRPCGQPVYSSLLKGGKCKSKTKKSPVPVR 298
 Db 237 CSKSGTGLSTRTVNDNPECLRVKTRICEVRPCGQPVYSSLLKGGKCKSKTKKSPVPVR 296
 QY 299 TYAGCLSVKYPKYPKYGCGVDCRCCTPQTRTVKMRFCEDGETFSKNVMMIOSCKNCYN 358
 Db 297 TYAGCSSVKKYPKYPKYGCGVDCRCCTPQTRTVKMRFCEDGETFSKNVMMIOSCKNCYN 356
 QY 359 CPHANEAFPPYRLFNDIHKFRD 381
 Db 357 CPHNEASFRLYSLFNDIHKFRD 379

RESULT 3
 CE10_CHICK
 ID CE10_CHICK STANDARD; PRT; 375 AA.
 AC P19336;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE CEF-10 PROTEIN PRECURSOR.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 OC Gallus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-89145206; PubMed-2537491;
 RA Simmons D.L., Levy D.B., Yannoni Y., Erikson R.L.;
 RT Identification of a phorbol ester-repressible v-src-inducible gene.;
 RL Proc. Natl. Acad. Sci. U.S.A. 86:1178-1182(1989).
 CC -!- FUNCTION: PROBABLE SECRETED REGULATORY PROTEIN.
 CC -!- INDUCTION: BY V-SRC.
 CC -!- SIMILARITY: BELONGS TO THE INSULIN-LIKE GROWTH FACTOR BINDING
 CC PROTEIN FAMILY. CEF-10/CYR61/CTFG/FISP-12/NOV PROTEIN SUBFAMILY.
 CC -!- SIMILARITY: CONTAINS 1 WFPC DOMAIN.
 CC -!- SIMILARITY: CONTAINS 1 C-TERMINAL CYSTINE KNOT-LIKE DOMAIN (CTCK).
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; J04496; AAA48661.1;
 CC PIR; A41428; A41428.
 CC INTERPRO; IPR000359;
 CC INTERPRO; IPR000867;
 CC INTERPRO; IPR000884;
 CC INTERPRO; IPR001007;
 CC PFAM; PF000007; Cys_knot; 1.
 CC PFAM; PF00219; IgFBP; 1.
 CC PFAM; PF00090; tsp_1; 1.
 CC PFAM; PF00093; vwc; 1.
 CC PROSITE; PS00222; IGF_BINDING; 1.
 CC PROSITE; PS01185; CTCK_1; 1.
 CC PROSITE; PS01225; CTCK_2; 1.
 CC PROSITE; PS01208; WFPC; 1.
 CC Growth factor binding; signal.
 CC SIGNAL 1 22

FT CHAIN 23 375 CEF-10 PROTEIN.
 FT DOMAIN 98 164
 FT CTCK 355
 FT DISULFID 281 318 BY SIMILARITY.
 FT DISULFID 298 332 BY SIMILARITY.
 FT DISULFID 309 348 BY SIMILARITY.
 FT DISULFID 312 350 BY SIMILARITY.
 FT DISULFID 317 354 BY SIMILARITY.
 SQ SEQUENCE 375 AA; 40651 MW; 95F2853BE35D5AE CRC64;

Query Match 80.3%; Score 1699; DB 1; Length 375;
 Best Local Similarity 81.2%; Pred. No. 1-7e-122;
 Matches 312; Conservative 19; Mismatches 41; Indels 12; Gaps 7;

QY 1 MSSRIARALAVVTLHLRLAL-STCPAACHCPLKAPGVGLVRDGGCGCKYCAQ 59
 Db 1 MSAGARP-ALAAALICLARLALGSPCAVQCQPAAPQCAPGVGLVPDGGCGCKYCAQ 59
 QY 60 LNEDESKTQPCDHTKGLGECNFGASSTALGICRAQSEGRPCPEYNSRIYQNGESFPNCKH 119
 Db 60 LNEDESKTQPCDHTKGLGECNFGASSTALGICRAQSEGRPCPEYNSRIYQNGESFPNCKH 119
 QY 120 QCTCIDGAVGCIPLCPQELSLPGLGCPNPLVKTGQCCCEWVCDSDSIKDPMEDQDGL 179
 Db 120 QCTCIDGAVGCIPLCPQELSLPGLGCPNPLVKTGQCCCEWVCDSDSIKDPMEDQDGL 179
 QY 180 GKELGFDASEVELTRNNELIAGVKGSSLKRLPVFGMEPRILYNPLQKQCIQVQTTWS 237
 Db 178 SKFGLDASEVELTRNNELIAGVKGSSLKRLPVFGMEPRILYNPLQKQCIQVQTTWS 237
 QY 238 QSKTCGTGISTRTVNDNPECLRVKTRICEVRPCGQPVYSSLLKGGKCKSKTKKSPVPVR 297
 Db 233 QSKTCGTGISTRTVNDNPECLRVKTRICEVRPCGQPVYSSLLKGGKCKSKTKKSPVPVR 292
 QY 298 FTYAGCLSVKYPKYPKYGCGVDCRCCTPQTRTVKMRFCEDGETFSKNVMMIOSCKNCY 357
 Db 293 FTYAGCSSVKKYPKYPKYGCGVDCRCCTPQTRTVKMRFCEDGETFSKNVMMIOSCKNCY 352
 QY 358 NCPHANEAFPPYRLFNDIHKFRD 381
 Db 353 NCPHANEAFPPYRLFNDIHKFRD 375

RESULT 4
 CTGF_MOUSE
 ID CTGF_MOUSE STANDARD; PRT; 348 AA.
 AC P29268;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE CONNECTIVE TISSUE GROWTH FACTOR PRECURSOR (CTGF) (FISP-12 PROTEIN).
 GN CTGF OR FISP12 OR FISP-12.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-91363290; PubMed-1888698;
 RA Rybeck R.-P., Macdonald-Bravo H., Mattei M.-G., Bravo R.;
 RT Structure, mapping, and expression of fisp-12, a growth factor-
 RT inducible gene encoding a secreted cysteine-rich protein.;
 RL Cell Growth Differ. 2:225-233(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-91229699; PubMed-2029337;
 RA Brunner A., Chinn J., Neubauer M.G., Purchio A.F.;
 RT Identification of a gene family regulated by transforming growth
 RT factor-beta.;
 RL DNA Cell Biol. 10:293-300(1991).
 CC -!- TISSUE SPECIFICITY: TESTIS, SPLEEN, KIDNEY, LUNG, HEART, AND BRAIN
 CC (LOWEST LEVEL IN TESTIS AND HIGHEST IN LUNG).
 CC -!- INDUCTION: BY GROWTH FACTORS.